RAW SEQUENCE LISTING

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Application Serial Number: 08/765,108
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/765,108*

This Raw Listing contains the General Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:
(i) APPLICANT: Massachusetts Institute of Technology
(ii) TITLE OF INVENTION: Class BI and CI Scavenger Receptors
(iii) NUMBER OF SEQUENCES: 8
(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Patrea L. Pabst
(B) STREET: 2800 One Atlantic Center
1201 West Peachtree Street
(C) CITY: Atlanta
(D) STATE: Georgia
(E) COUNTRY: USA
(F) ZIP: 30309-3450
(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/765,108
(B) FILING DATE: 27-MAR-1997
(C) CLASSIFICATION:
(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/US95/07721
(B) FILING DATE: 19-JUN-1995
(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Pabst, Patrea L.
(B) REGISTRATION NUMBER: 31,284
(C) REFERENCE/DOCKET NUMBER: MIT6620
(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (404) 873-8794
(B) TELEFAX: (404) 873-8795
(2) INFORMATION FOR SEQ ID NO:1:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(x) PUBLICATION INFORMATION:
(A) AUTHORS: Ashkenas, et al.
(C) JOURNAL: J. Lipid Res.
(D) VOLUME: 34

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47              (F) PAGES: 983-1000
48              (G) DATE: 1993
49              (K) RELEVANT RESIDUES IN SEQ ID NO:1: FROM 1 TO 20
50
51      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
52
53  AATGAAGAAC TGCTTAGTTT                                                20
54
55  (2) INFORMATION FOR SEQ ID NO:2:
56       (i) SEQUENCE CHARACTERISTICS:
57              (A) LENGTH: 18 base pairs
58              (B) TYPE: nucleic acid
59              (C) STRANDEDNESS: single
60              (D) TOPOLOGY: linear
61      (ii) MOLECULE TYPE: DNA
62     (iii) HYPOTHETICAL: NO
63      (iv) ANTI-SENSE: NO
64       (x) PUBLICATION INFORMATION:
65              (A) AUTHORS: Ashkenas, et al.
66              (C) JOURNAL: J. Lipid Res.
67              (D) VOLUME: 34
68              (F) PAGES: 983-1000
69              (G) DATE: 1993
70              (K) RELEVANT RESIDUES IN SEQ ID NO:1: FROM 1 TO 18
71
72      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
73
74  AATCAAGGAA TTTAACTG                                                  18
75
76  (2) INFORMATION FOR SEQ ID NO:3:
77       (i) SEQUENCE CHARACTERISTICS:
78              (A) LENGTH: 1788 base pairs
79              (B) TYPE: nucleic acid
80              (C) STRANDEDNESS: double
81              (D) TOPOLOGY: linear
82      (ii) MOLECULE TYPE: cDNA
83     (iii) HYPOTHETICAL: NO
84      (iv) ANTI-SENSE: NO
85      (ix) FEATURE:
86              (A) NAME/KEY: misc_feature
87              (B) LOCATION: 156..1683
88              (D) OTHER INFORMATION: /function= "Nucleotides 156 through
89              1683 encode the amino acid sequence for the Hamster
90              Scavenger Receptor Class B-I."
91
92      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
93
94  GCCACCTGCA GGGCTACTGC TGCTCCGGCC ACTGCCTGAG ACTCACCTTG CTGGAACGTG     60
95
96  AGCCTCGGCT TCTGTCATCT CTGTGGCCTC TGTCGCTTCT GTCGCTGTCC CCCTTCAGTC    120
97
98  CCTGAGCCCC GCGAGCCCGG GCCGCACACG CGGACATGGG CGGCAGCGCC AGGGCGCGCT    180
99
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100  GGGTGGCGGT GGGGCTGGGC GTCGTGGGGC TGCTGTGCGC TGTGCTCGGT GTGGTTATGA   240
101
102  TCCTCGTGAT GCCCTCGCTC ATCAAACAGC AGGTACTGAA GAATGTCCGC ATAGACCCCA   300
103
104  GCAGCCTGTC CTTTGCAATG TGGAAGGAGA TCCCTGTACC CTTCTACTTG TCCGTCTACT   360
105
106  TCTTCGAGGT GGTCAATCCC AGCGAGATCC TAAAGGGTGA GAAGCCAGTA GTGCGGGAGC   420
107
108  GTGGACCCTA TGTCTACAGG GAATTCAGAC ATAAGGCCAA CATCACCTTC AATGACAATG   480
109
110  ATACTGTGTC CTTTGTGGAG CACCGCAGCC TCCATTTCCA GCCGGACAGG TCCCACGGCT   540
111
112  CTGAGAGTGA CTACATTATA CTGCCTAACA TTCTGGTCTT GGGGGGCGCA GTAATGATGG   600
113
114  AGAGCAAGTC TGCAGGCCTG AAGCTGATGA TGACCTTGGG GCTGGCCACC TTGGGCCAGC   660
115
116  GTGCCTTTAT GAACCGAACA GTTGGTGAGA TCCTGTGGGG CTATGAGGAT CCCTTCGTGA   720
117
118  ATTTTATCAA CAAATACTTA CCAGACATGT TCCCCATCAA GGGCAAGTTC GGCCTGTTTG   780
119
120  TTGAGATGAA CAACTCAGAC TCTGGGCTCT TCACTGTGTT CACGGGCGTC CAGAACTTCA   840
121
122  GCAAGATCCA CCTGGTGGAC AGATGGAATG GGCTCAGCAA GGTCAACTAC TGGCATTCAG   900
123
124  AGCAGTGCAA CATGATCAAT GGCACTTCCG GGCAGATGTG GGCACCATTC ATGACACCCC   960
125
126  AGTCCTCGCT GGAATTCTTC AGTCCGGAAG CCTGCAGGTC TATGAAGCTC ACCTACCATG  1020
127
128  ATTCAGGGGT GTTTGAAGGC ATCCCCACCT ATCGCTTCAC AGCCCCTAAA ACTTTGTTTG  1080
129
130  CCAATGGGTC TGTTTACCCA CCCAATGAAG GTTTCTGCCC GTGCCTTGAA TCCGGCATTC  1140
131
132  AAAATGTCAG CACTTGCAGG TTTGGTGCAC CCCTGTTTCT GTCACACCCT CACTTCTACA  1200
133
134  ATGCAGACCC TGTGCTATCA GAAGCCGTTC TGGGTCTGAA CCCTGACCCA AGGGAGCATT  1260
135
136  CTTTGTTCCT TGACATCCAT CCGGTCACTG GGATCCCCAT GAACTGTTCT GTGAAGTTGC  1320
137
138  AGATAAGCCT CTACATCAAA GCTGTCAAGG GCATTGGGCA AACAGGGAAG ATCGAGCCCG  1380
139
140  TGGTCCTCCC ATTGCTGTGG TTTGAGCAGA GCGGTGCCAT GGGCGGCGAG CCCCTGAACA  1440
141
142  CGTTCTACAC GCAGCTGGTG CTGATGCCCC AGGTACTTCA GTATGTGCAG TATGTGCTGC  1500
143
144  TGGGGCTGGG CGGCCTCCTG CTGCTGGTGC CCGTCATCTA CCAGTTGCGC AGCCAGGAGA  1560
145
146  AATGCTTTTT ATTTTGGAGT GGTAGTAAAA AGGGCTCGCA GGATAAGGAG GCCATTCAGG  1620
147
148  CCTACTCTGA GTCTCTGATG TCACCAGCTG CCAAGGGCAC GGTGCTGCAA GAAGCCAAGC  1680
149
150  TGTAGGGTCC CAAAGACACC ACGAGCCCCC CCAACCTGAT AGCTTGGTCA GACCAGCCAT  1740
151
152  CCAGCCCCTA CACCCCGCTT CTTGAGGACT CTCTCAGCGG ACAGTCGC               1788
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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 509 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..509
(D) OTHER INFORMATION: /function= "Amino acid sequence for the Hamster Scavenger Receptor Class B-I."

(ix) FEATURE:
(A) NAME/KEY: Domain
(B) LOCATION: 9..32
(D) OTHER INFORMATION: /note= "Putative transmembrane domain."

(ix) FEATURE:
(A) NAME/KEY: Domain
(B) LOCATION: 440..464
(D) OTHER INFORMATION: /note= "Putative transmembrane domain."

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 1..385
(D) OTHER INFORMATION: /note= "Positions 102-104, 108-110, 173-175, 212-214, 227-229, 255-257,310-312, 330-332 and 383-385 represent potential N-linked glycosylation sites."

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 21..470
(D) OTHER INFORMATION: /note= "The cysteines at positions 21, 251, 280, 321, 323, 334, 384 and 470 represent potential disulfide linkages."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Met Gly Gly Ser Ala Arg Ala Arg Trp Val Ala Val Gly Leu Gly Val
1               5                  10                  15

Val Gly Leu Leu Cys Ala Val Leu Gly Val Val Met Ile Leu Val Met
            20                  25                  30

Pro Ser Leu Ile Lys Gln Gln Val Leu Lys Asn Val Arg Ile Asp Pro
        35                  40                  45

Ser Ser Leu Ser Phe Ala Met Trp Lys Glu Ile Pro Val Pro Phe Tyr
    50                  55                  60

Leu Ser Val Tyr Phe Phe Glu Val Val Asn Pro Ser Glu Ile Leu Lys
65                  70                  75                  80
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206
207       Gly Glu Lys Pro Val Val Arg Glu Arg Gly Pro Tyr Val Tyr Arg Glu
208                       85                  90                  95
209
210       Phe Arg His Lys Ala Asn Ile Thr Phe Asn Asp Asn Asp Thr Val Ser
211                   100                 105                 110
212
213       Phe Val Glu His Arg Ser Leu His Phe Gln Pro Asp Arg Ser His Gly
214               115                 120                 125
215
216       Ser Glu Ser Asp Tyr Ile Ile Leu Pro Asn Ile Leu Val Leu Gly Gly
217           130                 135                 140
218
219       Ala Val Met Met Glu Ser Lys Ser Ala Gly Leu Lys Leu Met Met Thr
220       145                 150                 155                 160
221
222       Leu Gly Leu Ala Thr Leu Gly Gln Arg Ala Phe Met Asn Arg Thr Val
223                       165                 170                 175
224
225       Gly Glu Ile Leu Trp Gly Tyr Glu Asp Pro Phe Val Asn Phe Ile Asn
226                   180                 185                 190
227
228       Lys Tyr Leu Pro Asp Met Phe Pro Ile Lys Gly Lys Phe Gly Leu Phe
229               195                 200                 205
230
231       Val Glu Met Asn Asn Ser Asp Ser Gly Leu Phe Thr Val Phe Thr Gly
232           210                 215                 220
233
234       Val Gln Asn Phe Ser Lys Ile His Leu Val Asp Arg Trp Asn Gly Leu
235       225                 230                 235                 240
236
237       Ser Lys Val Asn Tyr Trp His Ser Glu Gln Cys Asn Met Ile Asn Gly
238                       245                 250                 255
239
240       Thr Ser Gly Gln Met Trp Ala Pro Phe Met Thr Pro Gln Ser Ser Leu
241                   260                 265                 270
242
243       Glu Phe Phe Ser Pro Glu Ala Cys Arg Ser Met Lys Leu Thr Tyr His
244               275                 280                 285
245
246       Asp Ser Gly Val Phe Glu Gly Ile Pro Thr Tyr Arg Phe Thr Ala Pro
247           290                 295                 300
248
249       Lys Thr Leu Phe Ala Asn Gly Ser Val Tyr Pro Pro Asn Glu Gly Phe
250       305                 310                 315                 320
251
252       Cys Pro Cys Leu Glu Ser Gly Ile Gln Asn Val Ser Thr Cys Arg Phe
253                       325                 330                 335
254
255       Gly Ala Pro Leu Phe Leu Ser His Pro His Phe Tyr Asn Ala Asp Pro
256                   340                 345                 350
257
258       Val Leu Ser Glu Ala Val Leu Gly Leu Asn Pro Asp Pro Arg Glu His
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/765,108*

DATE: 02/17/2006
TIME: 13:00:43

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